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BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING ERROR REPORT

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Application Serial Number: 09/964 678
Source: OIPE
Date Processed by STIC: 10/16/2001

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- FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
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OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/964,678

DATE: 10/16/2001
TIME: 15:50:12

Input Set : A:\PTO.txt
Output Set: N:\CRF3\10162001\I964678.raw

SEQUENCE LISTING

4 (1) GENERAL INFORMATION:

6 (i) APPLICANT: de la Monte, Suzanne
7 Wands, Jack R.
9 (ii) TITLE OF INVENTION: Transgenic Animals and Cell Lines for
10 Screening Drugs Effective for the Treatment or Prevention
11 of Alzheimer's Disease

13 (iii) NUMBER OF SEQUENCES: 14

15 (iv) CORRESPONDENCE ADDRESS:

16 (A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
17 (B) STREET: 1100 New York Ave., Suite 600
18 (C) CITY: Washington
19 (D) STATE: DC
20 (E) COUNTRY: USA
21 (F) ZIP: 20005-3934

23 (v) COMPUTER READABLE FORM:

24 (A) MEDIUM TYPE: Floppy disk
25 (B) COMPUTER: IBM PC compatible
26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

29 (vi) CURRENT APPLICATION DATA:

C--> 30 (A) APPLICATION NUMBER: ~~US/09/964,678~~ *OK*
C--> 31 (B) FILING DATE: 28-Sep-2001
32 (C) CLASSIFICATION:

34 (viii) ATTORNEY/AGENT INFORMATION:

35 (A) NAME: Esmond, Robert W.
36 (B) REGISTRATION NUMBER: 32,893
37 (C) REFERENCE/DOCKET NUMBER: 0609.4370000

39 (ix) TELECOMMUNICATION INFORMATION:

40 (A) TELEPHONE: 202-371-2600
41 (B) TELEFAX: 202-371-2540

44 (2) INFORMATION FOR SEQ ID NO: 1:

46 (i) SEQUENCE CHARACTERISTICS:

47 (A) LENGTH: 1442 base pairs
48 (B) TYPE: nucleic acid
49 (C) STRANDEDNESS: double
50 (D) TOPOLOGY: both

52 (ii) MOLECULE TYPE: cDNA

55 (ix) FEATURE:

56 (A) NAME/KEY: CDS
57 (B) LOCATION: 15..1139

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

62 TTTT TTTT TTTT TGAG ATG GAG TTT TCG CTC TTG TTG CCC AGG CTG GAG TGC 50
63 Met Glu Phe Ser Leu Leu Leu Pro Arg Leu Glu Cys
64 1 5 10 98
66 AAT GGC GCA ATC TCA GCT CAC CGC AAC CTC CGC CTC CCG GGT TCA AGC
67 Asn Gly Ala Ile Ser Ala His Arg Asn Leu Arg Leu Pro Gly Ser Ser

*Errored: "Old format
may only be used when
prior application date
precedes July 1, 1998"*

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Input Set : A:\PTO.txt
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68	15	20	25	146
70	GAT TCT CCT GCC TCA GCC TCC CCA GTA GCT GGG ATT ACA GGC ATG TGC			
71	Asp Ser Pro Ala Ser Ala Ser Pro Val Ala Gly Ile Thr Gly Met Cys			
72	30	35	40	194
74	ACC CAC GCT CGG CTA ATT TTG TAT TTT TTT TTA GTA GAG ATG GAG TTT			
75	Thr His Ala Arg Leu Ile Leu Tyr Phe Phe Leu Val Glu Met Glu Phe			
76	45	50	55	242
78	CTC CAT GTT GGT CAG GCT GGT CTC GAA CTC CCG ACC TCA GAT GAT CCC			
79	Leu His Val Gly Gln Ala Gly Leu Glu Leu Pro Thr Ser Asp Asp Pro			
80	65	70	75	290
82	TCC GTC TCG GCC TCC CAA AGT GCT AGA TAC AGG ACT GGC CAC CAT GCC			
83	Ser Val Ser Ala Ser Gln Ser Ala Arg Tyr Arg Thr Gly His His Ala			
84	80	85	90	338
86	CGG CTC TGC CTG GCT AAT TTT TGT GGT AGA AAC AGG GTT TCA CTG ATG			
87	Arg Leu Cys Leu Ala Asn Phe Cys Gly Arg Asn Arg Val Ser Leu Met			
88	95	100	105	386
90	TGC CCA AGC TGG TCT CCT GAG CTC AAG CAG TCC ACC TGC CTC AGC CTC			
91	Cys Pro Ser Trp Ser Pro Glu Leu Lys Gln Ser Thr Cys Leu Ser Leu			
92	110	115	120	434
94	CCA AAG TGC TGG GAT TAC AGG CGT GCA GCC GTG CCT GGC CTT TTT ATT			
95	Pro Lys Cys Trp Asp Tyr Arg Arg Ala Ala Val Pro Gly Leu Phe Ile			
96	125	130	135	482
98	TTA TTT TTT TTA AGA CAC AGG TGT CCC ACT CTT ACC CAG GAT GAA GTG			
99	Leu Phe Phe Leu Arg His Arg Cys Pro Thr Leu Thr Gln Asp Glu Val			
100	145	150	155	530
102	CAG TGG TGT GAT CAC AGC TCA CTG CAG CCT TCA ACT CCT GAG ATC AAG			
103	Gln Trp Cys Asp His Ser Ser Leu Gln Pro Ser Thr Pro Glu Ile Lys			
104	160	165	170	578
106	CAT CCT CCT GCC TCA GCC TCC CAA GTA GCT GGG ACC AAA GAC ATG CAC			
107	His Pro Pro Ala Ser Ala Ser Gln Val Ala Gly Thr Lys Asp Met His			
108	175	180	185	626
110	CAC TAC ACC TGG CTA ATT TTT ATT TTT ATT TTT AAT TTT TTG AGA CAG			
111	His Tyr Thr Trp Leu Ile Phe Ile Phe Ile Phe Asn Phe Leu Arg Gln			
112	190	195	200	674
114	AGT CTC AAC TCT GTC ACC CAG GCT GGA GTG CAG TGG CGC AAT CTT GGC			
115	Ser Leu Asn Ser Val Thr Gln Ala Gly Val Gln Trp Arg Asn Leu Gly			
117	205	210	215	722
119	TCA CTG CAA CCT CTG CCT CCC GGG TTC AAG TTA TTC TCC TGC CCC AGC			
120	Ser Leu Gln Pro Leu Pro Pro Gly Phe Lys Leu Phe Ser Cys Pro Ser			
121	225	230	235	770
123	CTC CTG AGT AGC TGG GAC TAC AGG CGC CCA CCA CGC CTA GCT AAT TTT			
124	Leu Leu Ser Ser Trp Asp Tyr Arg Arg Pro Pro Arg Leu Ala Asn Phe			
125	240	245	250	818
127	TTT GTA TTT TTA GTA GAG ATG GGG TTC ACC ATG TTC GCC AGG TTG ATC			
128	Phe Val Phe Leu Val Glu Met Gly Phe Thr Met Phe Ala Arg Leu Ile			
129	255	260	265	866
131	TTG ATC TCT GGA CCT TGT GAT CTG CCT GCC TCG GCC TCC CAA AGT GCT			
132	Leu Ile Ser Gly Pro Cys Asp Leu Pro Ala Ser Ala Ser Gln Ser Ala			
133	270	275	280	

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135 GGG ATT ACA GGC GTG AGC CAC CAC GCC CGG CTT ATT TTT AAT TTT TGT      914
136 Gly Ile Thr Gly Val Ser His His Ala Arg Leu Ile Phe Asn Phe Cys
137 285                               290                               295                               300
139 TTG TTT GAA ATG GAA TCT CAC TCT GTT ACC CAG GCT GGA GTG CAA TGG      962
140 Leu Phe Glu Met Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp
141                               305                               310                               315
143 CCA AAT CTC GGC TCA CTG CAA CCT CTG CCT CCC GGG CTC AAG CGA TTC      1010
144 Pro Asn Leu Gly Ser Leu Gln Pro Leu Pro Pro Gly Leu Lys Arg Phe
145                               320                               325                               330
147 TCC TGT CTC AGC CTC CCA AGC AGC TGG GAT TAC GGG CAC CTG CCA CCA      1058
148 Ser Cys Leu Ser Leu Pro Ser Ser Trp Asp Tyr Gly His Leu Pro Pro
149                               335                               340                               345
151 CAC CCC GCT AAT TTT TGT ATT TTC ATT AGA GGC GGG GTT TCA CCA TAT      1106
152 His Pro Ala Asn Phe Cys Ile Phe Ile Arg Gly Gly Val Ser Pro Tyr
153                               350                               355                               360
155 TTG TCA GGC TGG TCT CAA ACT CCT GAC CTC AGG TGACCCACCT GCCTCAGCCT      1159
156 Leu Ser Gly Trp Ser Gln Thr Pro Asp Leu Arg
157 365                               370                               375
159 TCCAAAGTGC TGGGATTACA GGCGTGAGCC ACCTCACCCA GCCGGCTAAT TTAGATAAAA      1219
161 AAATATGTAG CAATGGGGGG TCTTGCTATG TTGCCCAGGC TGGTCTCAAA CTTCTGGCTT      1279
163 CATGCAATCC TTCCAAATGA GCCACAACAC CCAGCCAGTC ACATTTTTTTA AACAGTTACA      1339
165 TCTTTATTTT AGTATACTAG AAAGTAATAC AATAAACATG TCAAACCTGC AAATTCAGTA      1399
167 GTAACAGAGT TCTTTTATAA CTTTTAAACA AAGCTTTAGA GCA      1442
170 (2) INFORMATION FOR SEQ ID NO: 2:
172     (i) SEQUENCE CHARACTERISTICS:
173         (A) LENGTH: 375 amino acids
175         (B) TYPE: amino acid
176         (D) TOPOLOGY: linear
178     (ii) MOLECULE TYPE: protein
180     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
182 Met Glu Phe Ser Leu Leu Leu Pro Arg Leu Glu Cys Asn Gly Ala Ile
183 1                               5                               10                               15
185 Ser Ala His Arg Asn Leu Arg Leu Pro Gly Ser Ser Asp Ser Pro Ala
186                               20                               25                               30
188 Ser Ala Ser Pro Val Ala Gly Ile Thr Gly Met Cys Thr His Ala Arg
189                               35                               40                               45
191 Leu Ile Leu Tyr Phe Phe Leu Val Glu Met Glu Phe Leu His Val Gly
192                               50                               55                               60
194 Gln Ala Gly Leu Glu Leu Pro Thr Ser Asp Asp Pro Ser Val Ser Ala
195 65                               70                               75                               80
197 Ser Gln Ser Ala Arg Tyr Arg Thr Gly His His Ala Arg Leu Cys Leu
198                               85                               90                               95
200 Ala Asn Phe Cys Gly Arg Asn Arg Val Ser Leu Met Cys Pro Ser Trp
201                               100                              105                              110
203 Ser Pro Glu Leu Lys Gln Ser Thr Cys Leu Ser Leu Pro Lys Cys Trp
204                               115                              120                              125
206 Asp Tyr Arg Arg Ala Ala Val Pro Gly Leu Phe Ile Leu Phe Phe Leu
207                               130                              135                              140
209 Arg His Arg Cys Pro Thr Leu Thr Gln Asp Glu Val Gln Trp Cys Asp

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/964,678

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Input Set : A:\PTO.txt
Output Set: N:\CRF3\10162001\I964678.raw

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210 145                               150                               155                               160
212 His Ser Ser Leu Gln Pro Ser Thr Pro Glu Ile Lys His Pro Pro Ala
213                               165                               170                               175
215 Ser Ala Ser Gln Val Ala Gly Thr Lys Asp Met His His Tyr Thr Trp
216                               180                               185                               190
218 Leu Ile Phe Ile Phe Ile Phe Asn Phe Leu Arg Gln Ser Leu Asn Ser
219                               195                               200                               205
221 Val Thr Gln Ala Gly Val Gln Trp Arg Asn Leu Gly Ser Leu Gln Pro
222                               210                               215                               220
224 Leu Pro Pro Gly Phe Lys Leu Phe Ser Cys Pro Ser Leu Leu Ser Ser
225 225                               230                               235                               240
227 Trp Asp Tyr Arg Arg Pro Pro Arg Leu Ala Asn Phe Phe Val Phe Leu
228                               245                               250                               255
230 Val Glu Met Gly Phe Thr Met Phe Ala Arg Leu Ile Leu Ile Ser Gly
231                               260                               265                               270
233 Pro Cys Asp Leu Pro Ala Ser Ala Ser Gln Ser Ala Gly Ile Thr Gly
234                               275                               280                               285
236 Val Ser His His Ala Arg Leu Ile Phe Asn Phe Cys Leu Phe Glu Met
237                               290                               295                               300
239 Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp Pro Asn Leu Gly
240 305                               310                               315                               320
242 Ser Leu Gln Pro Leu Pro Pro Gly Leu Lys Arg Phe Ser Cys Leu Ser
243                               325                               330                               335
245 Leu Pro Ser Ser Trp Asp Tyr Gly His Leu Pro Pro His Pro Ala Asn
246                               340                               345                               350
248 Phe Cys Ile Phe Ile Arg Gly Gly Val Ser Pro Tyr Leu Ser Gly Trp
249                               355                               360                               365
251 Ser Gln Thr Pro Asp Leu Arg
252                               370                               375
254 (2) INFORMATION FOR SEQ ID NO: 3:
256 (i) SEQUENCE CHARACTERISTICS:
257 (A) LENGTH: 1381 base pairs
258 (B) TYPE: nucleic acid
259 (C) STRANDEDNESS: double
260 (D) TOPOLOGY: both
262 (ii) MOLECULE TYPE: cDNA
267 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
269 TTTTTTTTTT GAGATGGAGT TTTCGCTCTT GTTGCCCAGG CTGGAGTGCA ATGGCGCAAT 60
271 CTCAGCTCAC CGCAACCTCC GCCTCCCGGG TTCAAGCGAT TCTCCTGCCT CAGCCTCCCC 120
273 AGTAGCTGGG ATTACAGGCA TGTGCACCAC GCTCGGCTAA TTTTGTATTT TTTTTTAGTA 180
275 GAGATGGAGT TTAACCTCAT GTTGGTCAGG CTGGTCTCGA ACTCCCGACC TCAGATGATC 240
277 TCCCGTCTCG GCCTGCCCAA AGTGCTGAGA TTACAGGCAT GAGCCACCAT GCCCGGCCCTC 300
279 TGCCTGGCTA ATTTTGTGG TAGAAACAGG GTTTCACCTGA TGTTGCCCAA GCTGGTCTCC 360
281 TGAGCTCAAG CAGTCCACCT GCCTCAGCCT CCCAAAGTGC TGGGATTACA GGCGTCAGCC 420
283 GTGCCTGGCC TTTTATTTT ATTTTATTTT AGACACAGGT GTACCACTCT TACCCAGGAT 480
285 GAAGTGCAGT GGTGTGATCA CAGCTCACTG CAGCCTTCAA CTCCTGAGAT CAAGCAATCC 540
287 TCCTGCCTCA GCCTCCCAAG TAGCTGGGAC CAAAGACATG CACCACTACA CCTGGTAATT 600
289 TTTATTTTTA TTTTAATTT TTTGAGACAG AGTCTCACTC TGTCACCCAG GCTGGAGTGC 660
291 AGTGGCGCAA TCTTGCTCA CTGCAACCTC TGCCTCCCGG GTTCAAGTTA TTCTCCTGCC 720

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/964,678

DATE: 10/16/2001
TIME: 15:50:12

Input Set : A:\PTO.txt
Output Set: N:\CRF3\10162001\I964678.raw

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293 CCAGCCTCCT GAGTAGCTGG GACTACAGGC GCCCACCACG CCTAGCTAAT TTTTGTAT 780
295 TTTTAGTAGA GATGGGGTTT CACCATGTTC GCCAGGTGA TCTTGATCTC TTGACCTTGT 840
297 GATCTGCCTG CCTCGGCCTA CCCAAAGTGC TGGGATTACA GGTCGTGACT CCACGCCGGC 900
299 CTATTTTAA TTTTGTGTTG TTTGAAATGG AATCTCACTC TGTTACCCAG GTCGGAGTGC 960
301 AATGGCAAAT CTCGGCTACT CGCAACCTCT GCCTCCCGGG TCAAGCGATT CTCCTGTCTC 1020
303 AGCCTCCCAA GCAGCTGGGA TTACGGGACC TGCACCACAC CCCGCTAATT TTTGTATTTT 1080
305 CATTAGAGGC GGGTTTACCA TATTTGTCAG GCTGGGTCTC AAACCTCTGA CCTCAGGTGA 1140
307 CCCACCTGCC TCAGCCTTCC AAAGTGCTGG GATTACAGGC GTGAGCCACC TCACCCAGCC 1200
309 GGCTAATTTG GAATAAAAAA TATGTAGCAA TGGGGGTCTG CTATGTTGCC CAGGCTGGTC 1260
311 TCAAACTTCT GGCTTCAGTC AATCCTTCCA AATGAGCCAC AACACCCAGC CAGTCACATT 1320
313 TTTTAAACAG TTACATCTTT ATTTTAGTAT ACTAGAAAGT AATACAATAA ACATGTCAAA 1380
315 C
317 (2) INFORMATION FOR SEQ ID NO: 4:
319 (i) SEQUENCE CHARACTERISTICS:
320 (A) LENGTH: 1418 base pairs
321 (B) TYPE: nucleic acid
322 (C) STRANDEDNESS: both
323 (D) TOPOLOGY: both
325 (ii) MOLECULE TYPE: cDNA
330 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
332 TTTTTTTTTT GAGATGGAGT TTTGCTCTT GTTGCCAGG CTGGAGTGCA ATGGCGCAAT 60
334 CTCAGCTCAC CGCAACCTCC GCCTCCCGGG TTCAAGCGAT TCTCCTGCCT CAGCCTCCCC 120
336 AGTAGGCTGG GATTACAGGC ATGTGCACCA CGCTCGGCTA ATTTTGTATT TTTTTTTAGT 180
338 AGAGATGGAG TTTCTCCATG TTGGTCAGGC TGGTCTCGAA CTCCGACCTC AGATGATCCT 240
340 CCCGTCTCGG CCTCCCAAAG TGCTAGATAC AGGACTGAGC ACCATGCCCC GCCTCTGCCT 300
342 GGCTAATTTT TGTGGTAGAA ACAGGGTTTC ACTGATGTGC CCAAGCTGGT CTCCTGAGCT 360
344 CAAGCAGTCC ACCTGCCTCA GCCTCCCAA GTGCTGGGAT TACAGGCGTG CAGCCGTGCC 420
346 TGGCCTTTTT ATTTTATTTT TTTTAAGACA CAGGTGTCCC ACTCTTACCC AGGATGAAGT 480
349 GCAGTGGTGT GATCACAGCT CACTGCAGCC TTCAACTCTG AGATCAAGCA TCCTCCTGCC 540
351 TCAGCCTCCC AAAGTAGCTG GGACCAAAGA CATGCACCAC TACACCTGGC TAATTTTTAT 600
353 TTTTATTTTT AATTTTTTGA GACAGAGTCT CAACTCTGTC ACCCAGGCTG GAGTGCAGTG 660
355 GCGCAATCTT GGCTCACTGC AACCTCTGCC TCCCGGGTTC AAGTTATTCT CCTGCCCCAG 720
357 CCTCCTGAGT AGCTGGGACT ACAGGCGCCC ACCACGCCTA GCTAATTTTT TTGTATTTTT 780
359 AGTAGAGATG GGGTTTCACC ATGTTCGCCA GGTGATGCT AGATCTCTTG ACCTTGTGAT 840
361 CTGCCTGCCT CGGCCTCCCA AAGTGCTGGG ATTACAGGAC GTGACGCCCC CCGCCCGGCC 900
363 TATTTTTAAT TTTTGTGTTG TTGAAATGGA ATCTCACTCT GTTACCCAGG CTGGAGTGCA 960
365 ATGGCCAAAT CTCGGCTCAC TGCAACCTCT GCCTCCCGGG CTCAAGCGAT TCTCCTGTCT 1020
367 CAGCCTCCCA AGCAGCTGGG ATTACGGGCA CCTGCACCAC ACCCGCTAA TTTTGTATT 1080
369 TTCATTAGAG GCGGGGTTTC ACCATATTTG TCAGGCTGGT CTCAAACCTC TGACCTCAGG 1140
371 TGACCCACCT GCCTCAGCCT TCCAAAGTGC TGGGATTACA GGCGTGACGC CTCACCCAGC 1200
373 CGGCTAATTT AGATAAAAAA ATATGTAGCA ATGGGGGGTC TTGCTATGTT GCCCAGGCTG 1260
375 GTCTCAAACT TCTGGCTTCA TGCAATCCTT CCAAATGAGC CACAACACCC AGCCAGTCAC 1320
377 ATTTTAAAC AGTTACATCT TTATTTTAGT ATACTAGAAA GTGATACGAT AACATGGCGG 1380
379 AACCTGCAAA TTCGAGTAGT ACAGAGTCTT TTATAACT 1418
381 (2) INFORMATION FOR SEQ ID NO: 5:
383 (i) SEQUENCE CHARACTERISTICS:
384 (A) LENGTH: 22 base pairs
385 (B) TYPE: nucleic acid
386 (C) STRANDEDNESS: single

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/964,678

DATE: 10/16/2001

TIME: 15:50:13

Input Set : A:\PTO.txt

Output Set: N:\CRF3\10162001\I964678.raw

L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]